Youfang Cao, PhD

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Theoretical Biology and Biophysics (T-6)
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EDUCATION

Shanghai Jiao Tong University
Ph.D. in Biomedical Engineering   **2011**
Dissertation: "Theoretical modeling methods of stochastic biological networks and their applications", Advisor: Jie Liang
Honor: Anthony James Leggett and Haruko Kinase-Leggett Graduate Awards

Shanxi University
M.S. in Biochemistry and Molecular Biology   **2002**
Minor: Bioinformatics
Area of Concentration: Microbial genomics analysis

Shanxi University
B.S. in Computational Mathematics   **1999**

RELATED EXPERIENCE

Los Alamos National Laboratory, Theoretical Biology and Biophysics (T-6), Center for Nonlinear Studies (CNLS)
Postdoc Research Associate   **2015/05-Present**
Research on viral dynamics in HIV and HCV infections based on clinical data and multi-scale stochastic modeling; Study regulatory mechanisms of stochastic biological networks through exact computation and efficient biased sampling.

University of Illinois at Chicago, Department of Bioengineering
Research Assistant Professor   **2012/09–2015/04**
Studied cell pattern formation using novel multi-scale mechano-geometric modeling methodology; Developed multi-buffer dCME method for direct solution of chemical master equation.

University of Illinois at Chicago, Department of Bioengineering
Postdoc Research Associate   **2011/09–2012/08**
Developed efficient Monte Carlo sampling method for rare events in biological networks;

University of Illinois at Chicago, Department of Bioengineering
Research Scholar   **2009/03–2011/08**

Developed finite buffer method for direct solutions of chemical master equation; Studied efficiency and stability of phage λ bistable lysogenic-lytic epigenetic switch.

Shanghai Jiao Tong University, Shanghai Center for Systems Biomedicine
Assistant Research Scientist   **2006/08–2011/08**
Design of data analysis system and pipelines for metagenomics study of human gut microbiota.

Shanghai Jiao Tong University, College of Agriculture and Biology
Assistant Research Scientist   **2002/08–2006/07**
Development of a novel prediction method for protein structural classes; Discovery of novel genes from EST databases important for plant stress responses.

RESEARCH AREAS AND INTERESTS

Mathematical and computational modeling of biological networks;
Stochastic control of genetic circuits of cellular fate;
Multi-scale modeling for tissue pattern formation;
Theoretical Immunology;
Computational systems biology**.**

GRANT PROPOSALS

XSEDE Startup Allocation   2015-2016
"Stochastic Control of HIV Latency-Reactivation and Viral/Immune System Dynamics"
Role: PI,   TG-BIO150068   50,000 service units   Awarded.

UIC Chancellor's Discovery Fund for Multidisciplinary Pilot Research 2015
"Dynamic multi-scale cell model for spatio-temporal tissue pattern in wound healing"
Role: PI   Awarded and declined.
This is a competitive campus wide grant competition. Only 4-5 applications are awarded each year. This award was declined as I left UIC.

NIH R21 1R21AR069177-01
"Dynamic multiscale cell model for spatio-temporal tissue pattern in wound healing"
Role: PI   Submitted.

MANUSCRIPTS IN REVIEW AND IN PREPARATION

1. **Youfang Cao**, Anna Terebus and Jie Liang **(2015).** State space truncation with quantified effects for accurate solution of discrete Chemical Master Equation. *Bulletin of Mathematical Biology*. **Revised**.

2. A. Ismael, W. Tian, N. Waszczak, X. Wang, **Y. Cao,** D. Suchkov, Eli Bar, M. V. Metodiev, J. Liang, R. Arkowitz, and D. E. Stone **(2016).** Gβ promotes receptor polarization and chemotropism by inhibiting receptor phosphorylation, *Science Signaling*. **In 2nd revision.**

3. **Youfang Cao**, Anna Terebus and Jie Liang **(2015).** Accurate Chemical Master Equation solution method with multi-finite buffers for time-evolving and steady state probability

landscapes and first passage times. ***SIAM: Multiscale Modeling and Simulation.*** **In review**.

4. **Youfang Cao**, Wei Tian and Jie Liang **(2015).** Reaction-coupling stochastic differential equation: an approximation to the Chemical Master Equation. ***Manuscript.***

5. **Youfang Cao,** Jieling Zhao, Luisa DiPietro, and Jie Liang **(2015).** Dynamic cellular pattern formation in regenerative wound healing of human skin. ***Manuscript.***

6. Jieling Zhao, **Youfang Cao**, and Jie Liang **(2016)**. Difference and relevance of mechanical and chemical microenvironment effects on re-epithelialization of human skin wound healing. ***Manuscript***.

7. **Youfang Cao**, Jessica Conway, and Alan Perelson **(2015)**. Post-treatment control of HIV-1 through immune check-point blockade. ***In preparation.***

8. **Youfang Cao**, Xue Lei, and Jie Liang **(2015).** Stochastic control of latency and activation in HIV-1 infected cells. ***In preparation***.

PUBLICATIONS (TOTAL 844 CITATIONS FROM GOOGLE SCHOLAR, H-INDEX: 13)

1. Sema Kachalo, Hammad Naveed, **Youfang Cao**, Jieling Zhao, and Jie Liang **(2015).** Mechanical Model of Geometric Cell and Topological Algorithm for Cell Dynamics from Single-Cell to Formation of Monolayered Tissues with Pattern. ***PLoS One.*** 2015; 10(5): e0126484. **(Cited by: 0)**

2. Anna Terebus, **Youfang Cao** and Jie Liang **(2014).** Exact Computation of Probability Landscape of Stochastic Networks of Single Input and Coupled Toggle Switch Modules. ***Conf Proc IEEE Eng Med Biol Soc***. Accepted. **(Cited by: 0)**

3. Wei Tian, **Youfang Cao**, Amber Ismael, David Stone and Jie Liang **(2014).** Roles of Regulated Internalization in the Polarization of Cell Surface Receptors. ***Conf Proc IEEE Eng Med Biol Soc***. Accepted. **(Cited by: 0)**

4. **Youfang Cao** and Jie Liang **(2013)**. Adaptively biased sequential importance sampling for rare events in reaction networks with comparison with exact solutions from finite buffer dCME method. ***Journal of Chemical Physics*** 139, 025101. **(Cited by: 0)**

5. **Youfang Cao**, Hammad Naveed, Claire Liang and Jie Liang **(2013)**. Modeling spatial population dynamics of stem cell lineage in wound healing and cancerogenesis. ***Conf Proc IEEE Eng Med Biol Soc***. 5550-5553. **(Cited by: 1)**

6. **Youfang Cao**, Claire Liang, Hammad Naveed, Yingzi Li, Meng Chen and Qing Nie **(2012)**. Modeling spatial population dynamics of stem cell lineage in tissue growth. ***Conf Proc IEEE Eng Med Biol Soc***. 5502–5505. **(Cited by: 4)**

7. Hongyuan Zhu, Tianqi Chen, Xue Lei, Wei Tian, **Youfang Cao** and Ping Ao **(2012)**. Understand the noise of CI expression in phage λ lysogeny. ***Control Conference (CCC), 31st Chinese***, 7432-7436. **(Cited by: 1)**

8. Xiaojun Zhang, Siqing Yue, Huihui Zhong, Weiying Hua, Ruijia Chen, **Youfang Cao**, Liping Zhao **(2011)**. A diverse bacterial community in an anoxic quinoline-degrading bioreactor determined by using pyrosequencing and clone library analysis. ***Applied microbiology and biotechnology***, 91(2), 425-434. **(Cited by: 22)**

9. **Youfang Cao**, Hsiao-Mei Lu and Jie Liang **(2010).** Probability landscape of heritable and robust epigenetic state of lysogeny in phage lambda. ***Proceedings of the National Academy of Sciences USA***, 107(43), 18445–18450. **(Cited by: 23)**

10. Chenhong Zhang, Menghui Zhang, Shengyue Wang, Ruijun Han, **Youfang Cao**, Weiying Hua, Yuejian Mao, Xiaojun Zhang, Xiaoyan Pang, Chaochun Wei, Guoping Zhao, Yan Chen and Liping Zhao **(2010)**. Interactions between gut microbiota, host genetics and diet relevant to development of metabolic syndromes in mice. ***The ISME Journal*** 4:232–241. **(Cited by: 157)**

11. **Youfang Cao** and Jie Liang **(2010).** Nonlinear Langevin model with product stochasticity for biological networks: the case of the Schnakenberg model. ***Journal of Systems Science and Complexity***, 23:896–905. **(Cited by: 1)**

12. **Youfang Cao** and Jie Liang **(2009).** Nonlinear coupling for improved stochastic network model: A study of Schnakenberg model. ***The Third International Symposium on Optimization and Systems Biology (OSB'09) ORSC & APORC*** 379–386. **(Cited by: 3)**

13. **Youfang Cao** and Jie Liang **(2008).** Optimal enumeration of state space of finitely buffered stochastic molecular networks and accurate computation of steady state landscape probability. ***BMC Systems Biology*** 2:30. **(Cited by: 28)**

14. **Youfang Cao**, Hsiao-Mei Lu, and Jie Liang **(2008).** Stochastic probability landscape model for switching efficiency, robustness, and differential threshold for induction of genetic circuit in phage lambda. ***Conf Proc IEEE Eng Med Biol Soc***. 1:611–614. **(Cited by: 6)**

15. **Youfang Cao** and Jie Liang **(2007).** An optimal algorithm for enumerating state space of stochastic molecular networks with small copy numbers of molecules. ***Conf Proc IEEE Eng Med Biol Soc***. 1:4599-4602. **(Cited by: 1)**

16. Kai-Jing Zuo, Jie Qin, Jing-Ya Zhao, Hua Ling, Li-Da Zhang, **Youfang Cao**, Ke-Xuan Tang **(2007)**. Over-expression GbERF2 transcription factor in tobacco enhances brown spots disease resistance by activating expression of downstream genes. ***Gene*** 391(1-2), 80-90. **(Cited by: 54)**

17. Jin Wang, Kai-Jing Zuo, Jie Qin, Lida Zhang, Lan Su, Junrong Liu, Hua Ling, Jing-Ya Zhao, **Youfang Cao**, Ke-Xuan Tang **(2007)**. Isolation and bioinformatics analyses of a COR413-like gene from Gossypium barbadense. ***Acta Physiologiae Plantarum*** 29(1), 1-9. **(Cited by: 4)**

18. Lida Zhang, Kaijing Zuo, Fei Zhang, **Youfang Cao**, Jiang Wang, Yidong Zhang, Xiaofen Sun, Kexuan Tang **(2006)**. Conservation of noncoding microsatellites in plants: implication for gene regulation. ***BMC genomics*** 7(1), 323. **(Cited by: 37)**

19. **Youfang Cao**, Shi Liu, Lida Zhang, Jie Qin, Jiang Wang and Kexuan Tang **(2006).** Prediction of protein structural class with Rough Sets. ***BMC Bioinformatics*** 7:20. **(Cited by: 110)**

20. Yidong Zhang, Zeyun Wang, Lida Zhang, **Youfang Cao**, Danfeng Huang, Kexuan Tang **(2006).** Molecular cloning and stress-dependent regulation of potassium channel gene in Chinese cabbage (Brassica rapa ssp. Pekinensis). ***Journal of Plant Physiology*** 163(9), 968-978. **(Cited by: 18)**

21. Lida Zhang, Shunwu Yu, **Youfang Cao**, Jiang Wang, Kaijing Zuo, Jie Qin, Kexuan Tang **(2006).** Distributional gradient of amino acid repeats in plant proteins. ***Genome*** 49 (8), 900-905. **(Cited by: 11)**

22. Jie Qin, Kaijing Zuo, Jingya Zhao, Hua Ling, **Youfang Cao**, Chengxiang Qiu, Fupeng Li, Xiaofen Sun and Kexuan Tang **(2006).** Overexpression of GbERF confers alteration of ethylene-responsive gene expression and enhanced resistance to Pseudomonas syringae in transgenic tobacco. ***Journal of Biosciences*** 31(2):255–263. **(Cited by: 17)**

23. Yidong Zhang, Zeyun Wang, Lida Zhang, **Youfang Cao**, Danfeng Huang, Kexuan Tang **(2006)**. Molecular cloning and stress-dependent regulation of a glutamine synthetase gene in Chinese cabbage. ***Russian Journal of Plant Physiology*** 53 (2), 231-237. **(Cited by: 2)**

24. Jiang Wang, Lida Zhang, Kai-Jing Zuo, Hong-Mei Qian, **Youfang Cao**, Kexuan Tang **(2006)**. Cloning and Expressional Studies of the Voltage‐dependent Anion Channel Gene from Brassica rapa L. ***Journal of Integrative Plant Biology*** 48 (2), 197-203. **(Cited by: 7)**

25. Guoan Shen, Yongzhen Pang, Weisheng Wu, Zhongxiang Deng, Lingxia Zhao, **Youfang Cao**, Xiaofen Sun, Kexuan Tang **(2006).** Cloning and characterization of a flavanone 3-hydroxylase gene from Ginkgo biloba. ***Bioscience Reports*** 26(1), 19-29. **(Cited by: 30)**

26. Lingxia Zhao, Jingfu Li, Yourong Chai, Guoyin Kai, **Youfang Cao**, Xiaofen Sun, Kexuan Tang **(2006).** Investigation on Genetic Relationship and Cross Compatibility of S. lycopersicoides and Lycopersicon. ***Pakistan Journal of Biological Sciences*** 9, 1160-1168. **(Cited by: 3)**

27. **Youfang Cao**, Lianjie Wang, Kexue Xu, Chunhai Kou, Yulei Zhang, Guifang Wei, Junjian He, Yunfang Wang and Liping Zhao **(2005).** Information theory-based algorithm for in silico prediction of PCR products with whole genomic sequences as templates. ***BMC Bioinformatics*** 6:190. **(Cited by: 12)**

28. Jie Qin, Jingya Zhao, Kaijing Zuo, **Youfang Cao**, Hua Ling, Xiaofen Sun, Kexuan Tang **(2004)**. Isolation and characterization of an ERF-like gene from Gossypium barbadense. ***Plant Science*** 167(6):1383–1389. **(Cited by: 26)**

29. Zhugang Li, Lingxia Zhao, Guoyin Kai, Shunwu Yu, **Youfang Cao**, Yongzhen Pang, Xiaofen Sun, Kexuan Tang **(2004)**. Cloning and expression analysis of a water stress-induced gene from Brassica oleracea. ***Plant Physiology and Biochemistry*** 42 (10), 789-794. **(Cited by: 8)**

30. Dongqin Tang, Hongmei Qian, Shunwu Yu, **Youfang Cao**, Zhihua Liao, Lingxia Zhao, Xiaofen Sun, Danfeng Huang, Kexuan Tang **(2004).** cDNA cloning and characterization of a new stress-responsive gene BoRS1 from Brassica oleracea var. acephala. ***Physiologia Plantarum*** 121(4):578-585. **(Cited by: 8)**

31. Lida Zhang, Dejun Yuan, Shunwu Yu, Zhugang Li, **Youfang Cao**, Zhiqi Miao, Hongmei Qian, Kexuan Tang **(2004).** Preference of simple sequence repeats in coding and non-coding regions of Arabidopsis thaliana. ***Bioinformatics*** 20 (7), 1081. **(Cited by: 82)**

32. Lingxia Zhao, Lixin Jin, Zhugang Li, **Youfang Cao**, Chengxiang Qiu, Dongqin Tang, Hongmei Qian, Kexuan Tang **(2004)**. Cloning and DNA sequence Analysis of Element

Responsive to Ethylene in E8 Promoter of the Tomato. *Acta Horticulturae Sinica* 31 (2), 204-208. **(Cited by: 1)**

33. Jingya Zhao, Kaijing Zuo, Jin Wang, **Youfang Cao**, Lida Zhang, Kexuan Tang **(2003).** cDNA cloning and characterization of a cotton peptide methionine sulfoxide reductase (cMsrA). *Mitochondrial DNA* 14 (4), 303-310. **(Cited by: 7)**

34. Yingchun Chen, **Youfang Cao**, Liping Zhao **(2002)**. Non-random nature of genomic DNA amplification of *E. coli* K-12 MG1655 via ERIC-PCR. *Microbiology China* (Chinese) 29 (6), 28-32. **(Cited by: 3)**

35. Youfang Cao, Liping Zhao **(2001)**. Computational analysis of the distribution of ERIC (IRU) in different bacterial genomes. *Journal of Shanxi University (Natural Science Edition)* (Chinese) 25 (4), 354-357. **(Cited by: 0)**

ORAL PRESENTATIONS

"Multistable Physiological States from Simple Stochastic Gene Regulatory Network Motifs"
<u>Invited Speaker</u> at 37th Annual International Conference of the IEEE
Engineering in Medicine & Biology Society, Milan, Italy   2015

"Using the Finite Buffer method (fb-dCME) to model stochastic viral dynamics"
<u>Lecturer</u> at The Ninth q-bio Summer School, Albuquerque, NM   2015

"Multiscale Simulation of Wound Healing with Dynamics Cell Model with Embedded Gene Networks"
<u>Invited Speaker</u> at 36th Annual International Conference of the IEEE
Engineering in Medicine & Biology Society, Chicago, IL   2014

"Multi-scale computational modeling of cellular processes: from genetic circuits to cell pattern formation"
<u>Invited talk</u> in Kean University, Union, NJ   2014

"Spatio-Temporal Dynamics of Cell Population in Models of Human Skin Wound Healing"
<u>Invited Speaker</u> at 35th Annual International Conference of the
IEEE Engineering in Medicine & Biology Society, Osaka, Japan   2013

"Modeling Spatial Population Dynamics of Stem Cell Lineage in Wound Healing and Cancerogenesis"
Paper presented at 35th Annual International Conference of the
IEEE Engineering in Medicine & Biology Society, Osaka Japan   2013

"Modeling Spatial Population Dynamics of Stem Cell Lineage in Wound Healing"
<u>Invited Speaker</u> at 34th Annual International Conference of the
IEEE Engineering in Medicine & Biology Society, San Diego, CA   2012

"Multiscale dynamic processes in biological systems: epigenetic circuits for lysogeny maintenance, cell signal responses, and tissue development."
<u>Invited presentation</u> at Department of Physics, University of Illinois
at Chicago   2012

"Modeling spatial population dynamics of stem cell in tissue growth and regeneration."

<u>Selected Presenter</u> at Regenerative Biology and Tissue
Engineering Workshop at University of Illinois, Urbana-Champaign   2011

"Computing probability landscapes of stochastic biological networks through discrete Chemical Master Equation: Maintenance of phage lambda epigenetic state."
The 21th International Conference on Genome Informatics (GIW
2010), Hangzhou, China   2010

CONFERENCE POSTERS

"Post-treatment control of HIV-1 and immune check-point blockade"
The Duke Center for HIV/AIDS Vaccine Immunology and
Immunogen Discovery (CHAVI-ID), Durham, NC   2015

"Stochastic Control of Intracellular Latency and Transactivation in Human Immunodeficiency Virus Type 1 (HIV-1)"
Biophysical Society Annual Meeting, Baltimore, MD   2015

"Spatio-temporal cell pattern formation during skin wound healing"
The Fourth Annual Meeting of the American College of
Wound Healing and Tissue Repair, Chicago, IL   2014

"Roles of Regulated Internalization in the Polarization of Cell Surface Receptors"
36th Annual International Conference of the IEEE
Engineering in Medicine & Biology Society, Chicago, IL   2014

"Multi-Finite Buffer Method for Direct Solution of Discrete Chemical Master Equation"
Biophysical Society Annual Meeting, San Francisco, CA   2014

"Role of Internalization of Cell Surface Receptors in Regulation of Cell Polarity"
Biophysical Society Annual Meeting, San Francisco, CA   2014

"Modeling Spatial Population Dynamics of Stem Cell Lineage in Tissue Growth"
Paper presented at 34th Annual International Conference of the
IEEE Engineering in Medicine & Biology Society, San Diego, CA   2012

"Stochastic temporal-spatial population dynamics of stem cell in tissue growth and regeneration"
Stem Cell and Regenerative Medicine, University of Illinois at
Chicago   2012

"Computing probabilistic landscape of stochastic network for maintenance of epigenetic states of cell and for regulation of cellular fate"
Ninth Annual Chicago Biomedical Consortium (CBC) Symposium   2011

"Cholesky-Langevin Model for Biochemical Networks with Accurate Account of Stochastic Effects of Couplings between Molecular Species"
Biophysical Society 54th Annual Meeting, San Francisco, CA   2010

"A Study of Cro's Role in the Induction of Phage Lambda Switch by Stochastic Probability Landscape Model"
Biophysical Society 53th Annual Meeting, Boston, MA   2009

"Stochastic probability landscape model for switching efficiency, robustness, and differential threshold for induction of genetic circuit in phage lambda"
Engineering in Medicine and Biology Society, 30th Annual
International Conference of the IEEE, Vancouver, BC, Canada   2008

"An optimal algorithm for enumerating state space of stochastic molecular networks with small copy numbers of molecules"
Engineering in Medicine and Biology Society, 29th Annual
International Conference of the IEEE, Lyon, France   2007

AWARDS

Travel Award for the 2015 Annual Computational Genomics Workshop
The Center for Cell Circuits at the Broad Institute.   2015

Anthony James Leggett and Haruko Kinase-Leggett Graduate Awards, First Place
Shanghai Jiao Tong University   2011

Selected Presenter at Regenerative Biology and Tissue Engineering Workshop
University of Illinois, Urbana-Champaign   2011

TEACHING AND MENTORING EXPERIENCES

Facilitator, BIOE 250 Clinical Problems in Bioengineering, University of Illinois at Chicago
1 contact hour/week for 1 semester.   2015

Student Research Advisor, Scientific Inquiry and Research Course, Illinois Mathematics and Science Academy (IMSA). Advising research of local high school student.
1 day/week for 48 weeks.   2011-2013

PROFESSIONAL MEMBERSHIPS

Society for Industrial and Applied Mathematics, Early Career Membership
American Association for the Advancement of Science
Biophysical Society, Early Career membership

JOURNAL REVIEWER

IEEE EMBC 2009, 2011, 2012, 2013, 2014, 2015
Journal of Theoretical Biology
Mathematical Biosciences
BMC Bioinformatics
BMC Systems Biology